# An application of the SIR model to epidemics in Portugal

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**Abstract** We apply the SIR model to study the evolution of Measles and Hepatitis *C* in Portugal using data from 1996 until 2007. Our results are potentially interesting to forecast the evolution of those viruses in subsequent years.

### 1 Introduction and the SIR model

The well-known SIR model was introduced by Kermack and McKendrick in 1927 (see e.g. [1, 4]) to study the propagation of epidemics. The model describes the dynamics of a population divided into three classes of individuals: susceptible (S), infected (I) and recovered (R). It assumes a spatially homogeneous population in each class (for  $S, I, R : \mathbb{R} \to \mathbb{R}$  of class  $C^1$ ) whose evolution is given by:

$$\begin{cases} \frac{dS}{dt} = (\lambda - \mu)S - \beta SI \\ \frac{dI}{dt} = \beta SI - (\mu + \alpha)I \\ \frac{dR}{dt} = \alpha I - \mu R, \qquad t \ge 0, \end{cases}$$
 (1)

where  $\alpha, \beta, \lambda, \mu \in \mathbb{R}^+$  and  $\lambda > \mu$  are, respectively, the disease death rate, the infection coefficient, the birth rate and the natural death rate. It is easy to see that the

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first two equations can be directly integrated to give:

$$(\lambda - \mu)(\ln I - \ln I_0) - \beta(I - I_0 + S - S_0) + (\mu + \alpha)(\ln S - \ln S_0) = 0$$
 (2)

where the subscript 0 denotes evaluation at t = 0. It turns out that I has extreme values, which are often used as indicators of the epidemics strenght [1], for

$$S=\frac{\mu+\alpha}{\beta}.$$

Despite the mathematical simplicity of the SIR model, it has been used in the past to study the evolution of epidemics in a variety of scenarios (see e.g. [1] and references therein).

## 2 Application to recent data of the portuguese health system

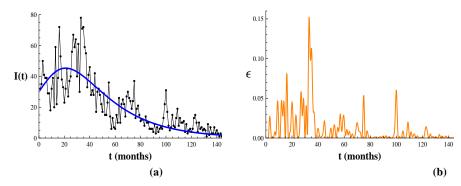
We have applied the SIR model briefly described in the previous section as a toy model to study the evolution of the Measels (M) and Hepatitis C (HC) in Portugal from 1996 until 2007. Part of this work is included in the master thesis of Correia [2]. The data we have studied was obtained from the webpage of the portuguese health system [3] and refers to *monthly* values of the number of infected individuals in each case. In order to find the best SIR fit to the data we have obtained numerically the optimal values for the parameters  $\alpha, \beta, \lambda$  and  $\mu$  corresponding to the minimum average error  $\varepsilon$  and maximum of the correlation coefficient r given by:

$$r^{2} = 1 - \frac{\sum_{j=1}^{N} (d_{j} - i_{j})^{2}}{\sum_{j=1}^{N} (d_{j} - \overline{d})^{2}}$$
(3)

where  $d_1, \ldots, d_N$  denote the observed values,  $i_1, \ldots, i_N$  the adjusted values and  $\overline{d}$  is the average of the observed values.

We found that the optimal values for the parameters are  $\alpha_M = 0.9$ ,  $\beta_M = 0.02$ ,  $\lambda_M = 0.09$ ,  $\mu_M = 0.01$  for the case of Measels, and  $\alpha_{HC} = 0.039$ ,  $\beta_{HC} = 0.001$ ,  $\lambda_{HC} = 0.006$ ,  $\mu_{HC} = 0.001$  for the case of Hepatitis C, which give  $r_M = 0.79$  and  $r_{HC} = 0.8$ , respectively. From the numerical integration of Eq. (1), referred to the dynamics of both Measels and Hepatitis C, we have found the fittings shown in Figure 1 and Figure 2. The left frames of these figures show the data for infected individuals and the curves obtained from the SIR model. The right frames show the corresponding error curves.

We have also considered *anual* data, and by performing a similar analysis, we have obtained  $\alpha_M = 0.9$ ,  $\beta_M = 0.002$ ,  $\lambda_M = 0.09$ ,  $\mu_M = 0.01$  and  $\alpha_{HC} = 0.24$ ,  $\beta_{HC} = 0.002$ ,  $\lambda_{HC} = 0.09$ ,  $\mu_{HC} = 0.01$ , which give  $r_M = 0.95$  and  $r_{HC} = 0.91$ . The



**Fig. 1** Monthly data – Hepatitis C. SIR model for  $\alpha = 0.039$ ,  $\beta = 0.001$ ,  $\lambda = 0.006$ ,  $\mu = 0.001$ . Curve of the model (a) and corresponding error curve (b).

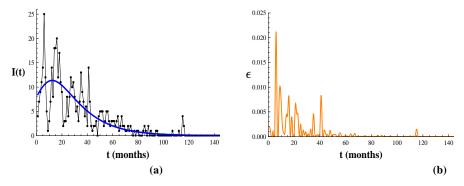


Fig. 2 Monthly data – Measles. SIR model for  $\alpha = 0.9$ ,  $\beta = 0.02$ ,  $\lambda = 0.09$  and  $\mu = 0.01$ . Curve of the model (a) and corresponding error curve (b).

dynamics is obtained from the numerical integration of the corresponding differential systems and is represented by the fittings shown in Figure 3.

The annual data shows lower volatility than the monthly data and therefore, as expected, we have found a better fitting for the former data translated into higher correlation coefficients.

In general, the web data from the portuguese health system [3] seems too scarce to make feasible predictions for the evolution of virus epidemics, although the particular case of Hepatitis C seem to be the one with more complete data. Thus, in this case, we have used our previous results to forecast the number of infected individuals for the four subsequent years using polynomial interpolation of 4th degree. For the years 2009 and 2011 we have obtained:

$$I_{HC}(2009) \sim 36$$
,  $I_{HC}(2011) \sim 15$ .

We conclude that although the SIR model (1) is quite simple and the 1996-2007 data from the portuguese health system is scarce, it can give us some useful insight about the evolution of the Measles and Hepatitis C viruses. In turn, this can be used



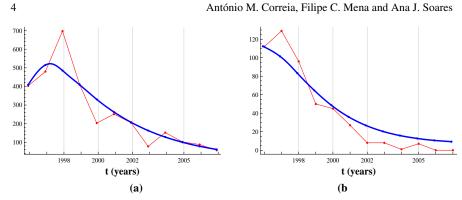


Fig. 3 Annual data – Infection early rates and approximation curve obtained from the SIR model. (a) Hepatitis C.  $\alpha = 0.24$ ,  $\beta = 0.002$ ,  $\lambda = 0.09$  and  $\mu = 0.01$ . (b) Measles -  $\alpha = 0.9$ ,  $\beta = 0.002$ ,  $\lambda = 0.002$ 0.09 and  $\mu = 0.01$ .

as a forecast for the number of infected individuals in subsequent years and we have applied this idea to forecast the evolution of Hepatitis C up to 2011.

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